



0570  
1007

## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 101226106C  
Source: C I P E  
Date Processed by STIC: 10/8/02

**THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.**

**PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:**

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

**TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:**

**<http://www.uspto.gov/web/offices/pac/checker>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

# Raw Sequence Listing Error Summary

01PE

## ERROR DETECTED

## SUGGESTED CORRECTION

SERIAL NUMBER: 10 026,106C

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 ☒ Wrapped Nucleics  
Wrapped Aminos  
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 ☐ Invalid Line Length  
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 ☒ Misaligned Amino  
Numbering  
The numbering under each 3<sup>rd</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 ☐ Non-ASCII  
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 ☐ Variable Length  
Sequence(s) \_\_\_\_\_ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 ☐ PatentIn 2.0  
"bug"  
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) \_\_\_\_\_. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 ☐ Skipped Sequences  
(OLD RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence:  
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
This sequence is intentionally skipped  
  
Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 ☐ Skipped Sequences  
(NEW RULES)  
Sequence(s) \_\_\_\_\_ missing. If intentional, please insert the following lines for each skipped sequence.  
<210> sequence id number  
<400> sequence id number  
000
- 9 ☐ Use of n's or Xaa's  
(NEW RULES)  
Use of n's and/or Xaa's have been detected in the Sequence Listing.  
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.
- 10 ☐ Invalid <213>  
Response  
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 ☐ Use of <220>  
Sequence(s) \_\_\_\_\_ missing the <220> "Feature" and associated numeric identifiers and responses.  
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 ☐ PatentIn 2.0  
"bug"  
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 ☐ Misuse of n  
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.



OIPE

**Does Not Comply**  
**Corrected Diskette Needed**

## RAW SEQUENCE LISTING

DATE: 10/08/2002

PATENT APPLICATION: US/10/026,106C

TIME: 13:59:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\10082002\J026106C.raw

1 <110> APPLICANT: Renauld, Jean-Christophe  
 2 Fickensicher, Helmut  
 3 Dumoutier, Laure  
 4 Hor, Simon  
 6 <120> TITLE OF INVENTION: Isolated Cytokine Receptor LICR-2  
 8 <130> FILE REFERENCE: LUD 5752 NDH  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/026,106C  
 12 <141> CURRENT FILING DATE: 2001-12-21  
 14 <160> NUMBER OF SEQ ID NOS: 19

## ERRORED SEQUENCES

104 <210> SEQ ID NO: 8  
 105 <211> LENGTH: 522  
 106 <212> TYPE: PRT  
 107 <213> ORGANISM: Homo sapiens  
 W--> 108 <220> FEATURE:  
 W--> 109 <400> SEQUENCE: 8

110	Met	Ala	Gly	Pro	Glu	Arg	Trp	Gly	Pro	Leu	Leu	Leu	Cys	Leu	Leu	Gln
111	1			5					10					15		
112	Ala	Ala	Pro	Gly	Arg	Pro	Arg	Leu	Ala	Pro	Pro	Gln	Asn	Val	Thr	Leu
113				20					25					30		
114	Leu	Ser	Gln	Asn	Phe	Ser	Val	Tyr	Leu	Thr	Trp	Leu	Pro	Gly	Leu	Gly
115			35					40					45			
116	Asn	Pro	Gln	Asp	Val	Thr	Tyr	Phe	Val	Ala	Tyr	Gln	Ser	Ser	Pro	Thr
117		50					55					60				
118	Arg	Arg	Arg	Trp	Arg	Glu	Val	Glu	Glu	Cys	Ala	Gly	Thr	Lys	Glu	Leu
119	65				70				75					80		
120	Leu	Cys	Ser	Met	Met	Cys	Leu	Lys	Lys	Gln	Asp	Leu	Tyr	Asn	Lys	Phe
E--> 121				85					90					95		
122	Lys	Gly	Arg	Val	Arg	Thr	Val	Ser	Pro	Ser	Ser	Lys	Ser	Pro	Trp	Val
E--> 123			100						105					110		
124	Glu	Ser	Glu	Tyr	Leu	Asp	Tyr	Leu	Phe	Glu	Val	Glu	Pro	Ala	Pro	Pro
E--> 125			115						120					125		
126	Val	Leu	Val	Leu	Thr	Gln	Thr	Glu	Glu	Ile	Leu	Ser	Ala	Asn	Ala	Thr
E--> 127		130						135					140			
128	Tyr	Gln	Leu	Pro	Pro	Cys	Met	Pro	Pro	Leu	Asp	Leu	Lys	Tyr	Glu	Val
E--> 129	145				150					155				160		
130	Ala	Phe	Trp	Lys	Glu	Gly	Ala	Gly	Asn	Lys	Thr	Leu	Phe	Pro	Val	Thr
E--> 131				165					170					175		
132	Pro	His	Val	Thr	Pro	His	Gly	Gln	Pro	Val	Gln	Ile	Thr	Leu	Gln	Pro
E--> 133				180					185					190		

*Amino numbering misaligned.  
See error summary sheet item 3*

## RAW SEQUENCE LISTING

DATE: 10/08/2002

PATENT APPLICATION: US/10/026,106C

TIME: 13:59:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\10082002\J026106C.raw

```

      134 Ala Ala Ser Glu His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe
E--> 135      195      200      205
      136 Ser Val Pro Lys Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu
E--> 137      210      215      220
      138 Glu Val Pro Glu Ala Asn Trp Ala Phe Leu Val Leu Pro Ser Leu Leu
E--> 139 225      230      235      240
      141 Ile Leu Leu Leu Val Ile Ala Ala Gly Gly Val Ile Trp Lys Thr Leu
E--> 142      245      250      255
      143 Met Gly Asn Pro Trp Phe Gln Arg Ala Lys Met Pro Arg Ala Leu Asp
E--> 144      260      265      270
      145 Phe Ser Gly His Thr Thr His Pro Val Ala Thr Phe Gln Pro Ser Arg
E--> 146      275      280      285
      147 Pro Glu Ser Val Asn Asp Leu Phe Leu Cys Pro Gln Lys Glu Leu Thr
E--> 148      290      295      300
      149 Arg Gly Val Arg Pro Thr Pro Arg Val Arg Pro Ala Thr Gln Gln Thr
E--> 150 305      310      315      320
      153 Arg Trp Lys Lys Asp Leu Ala Glu Asp Glu Glu Glu Glu Asp Thr Glu
E--> 154      325      330      335
      155 Asp Gly Val Ser Phe Gln Pro Tyr Ile Glu Pro Pro Ser Phe Leu Gly
E--> 156      340      345      350
      157 Gln Glu His Gln Ala Pro Gly His Ser Glu Ala Gly Gly Val Asp Ser
E--> 158      355      360      365
      159 Gly Arg Pro Arg Ala Pro Leu Val Pro Ser Glu Gly Ser Ser Ala Trp
E--> 160      370      375      380
      161 Asp Ser Ser Asp Arg Ser Trp Ala Ser Thr Val Asp Ser Ser Trp Asp
E--> 162 385      390      395      400
      163 Arg Ala Gly Ser Ser Gly Tyr Leu Ala Glu Lys Gly Pro Gly Gln Gly
E--> 164      405      410      415
      165 Pro Gly Gly Asp Gly His Gln Glu Ser Leu Pro Pro Pro Glu Phe Ser
E--> 166      420      425      430
      167 Lys Asp Ser Gly Phe Leu Glu Glu Leu Pro Glu Asp Asn Leu Ser Ser
E--> 168      435      440      445
      169 Trp Ala Thr Trp Gly Thr Leu Pro Pro Glu Pro Pro Asn Leu Val Pro
E--> 170      450      455      460
      172 Gly Gly Pro Pro Val Ser Leu Gln Thr Leu Thr Phe Cys Trp Glu Ser
E--> 173 465      470      475      480
      174 Ser Pro Glu Glu Glu Glu Ala Arg Glu Ser Glu Ile Glu Asp Ser
E--> 175      485      490      495
      176 Asp Ala Gly Ser Trp Gly Ala Glu Ser Thr Gln Arg Thr Glu Asp Arg
E--> 177      500      505      510
      178 Gly Arg Thr Leu Gly His Tyr Met Ala Arg      515
E--> 179      520
      220 <210> SEQ ID NO: 10
      221 <211> LENGTH: 244
      222 <212> TYPE: PRT
      223 <213> ORGANISM: Homo sapiens
W--> 224 <220> FEATURE:
W--> 225 <400> SEQUENCE: 10
      227 Met Ala Gly Pro Glu Arg Trp Gly Pro Leu Leu Leu Cys Leu Leu Gln

```

## RAW SEQUENCE LISTING

DATE: 10/08/2002

PATENT APPLICATION: US/10/026,106C

TIME: 13:59:24

Input Set : A:\EP.txt

Output Set: N:\CRF4\10082002\J026106C.raw

```

228 1          5          10          15
229 Ala Ala Pro Gly Arg Pro Arg Leu Ala Pro Pro Gln Asn Val Thr Leu
230          20          25          30
231 Leu Ser Gln Asn Phe Ser Val Tyr Leu Thr Trp Leu Pro Gly Leu Gly
232          35          40          45
233 Asn Pro Gln Asp Val Thr Tyr Phe Val Ala Tyr Gln Ser Ser Pro Thr
234          50          55          60
235 Arg Arg Arg Trp Arg Glu Val Glu Glu Cys Ala Gly Thr Lys Glu Leu
236 65          70          75          80
237 Leu Cys Ser Met Met Cys Leu Lys Lys Gln Asp Leu Tyr Asn Lys Phe
E--> 238          85          90          95
239 Lys Gly Arg Val Arg Thr Val Ser Pro Ser Ser Lys Ser Pro Trp Val
E--> 240          100          105          110
241 Glu Ser Glu Tyr Leu Asp Tyr Leu Phe Glu Val Glu Pro Ala Pro Pro
E--> 242          115          120          125
243 Val Leu Val Leu Thr Gln Thr Glu Glu Ile Leu Ser Ala Asn Ala Thr
E--> 244          130          135          140
245 Tyr Gln Leu Pro Pro Cys Met Pro Pro Leu Asp Leu Lys Tyr Glu Val
E--> 246 145          150          155          160
247 Ala Phe Trp Lys Glu Gly Ala Gly Asn Lys Thr Leu Phe Pro Val Thr
E--> 248          165          170          175
249 Pro His Gly Gln Pro Val Gln Ile Thr Leu Gln Pro Ala Ala Ser Glu
E--> 250          180          185          190
251 His His Cys Leu Ser Ala Arg Thr Ile Tyr Thr Phe Ser Val Pro Lys
E--> 252          195          200          205
253 Tyr Ser Lys Phe Ser Lys Pro Thr Cys Phe Leu Leu Glu Val Pro Gly
E--> 256          210          215          220
257 Leu Phe Trp Thr His Thr Pro Cys Gly Asn Leu Ser Ala Gln Gln Thr
E--> 258 225          230          235          240
259 Arg Val Arg Glu
294 <210> SEQ ID NO: 15
295 <211> LENGTH: 27
296 <212> TYPE: DNA
297 <213> ORGANISM: Homo sapiens
W--> 298 <220> FEATURE:
W--> 299 <400> SEQUENCE: 15
E--> 300 aatgtctaga tgctgttctc atttacc
301 (27)
313 <210> SEQ ID NO: 17
314 <211> LENGTH: 20
315 <212> TYPE: DNA
316 <213> ORGANISM: Homo sapiens
W--> 317 <220> FEATURE:
W--> 318 <400> SEQUENCE: 17
E--> 319 gtgaaatatt gctccgtcgt
320 (20)

```

*Handwritten notes:*

- From line 301 (27) to line 313: *Wrapped nucleic acids*
- From line 301 (27) to line 313: *See error summary sheet, item 1*
- From line 319 (20) to line 320: *same error*

## VERIFICATION SUMMARY

DATE: 10/08/2002

PATENT APPLICATION: US/10/026,106C

TIME: 13:59:25

Input Set : A:\EP.txt

Output Set: N:\CRF4\10082002\J026106C.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application Number  
L:20 M:283 W: Missing Blank Line separator, <220> field identifier  
L:21 M:283 W: Missing Blank Line separator, <400> field identifier  
L:28 M:283 W: Missing Blank Line separator, <220> field identifier  
L:29 M:283 W: Missing Blank Line separator, <400> field identifier  
L:36 M:283 W: Missing Blank Line separator, <220> field identifier  
L:37 M:283 W: Missing Blank Line separator, <400> field identifier  
L:44 M:283 W: Missing Blank Line separator, <220> field identifier  
L:45 M:283 W: Missing Blank Line separator, <400> field identifier  
L:54 M:283 W: Missing Blank Line separator, <220> field identifier  
L:55 M:283 W: Missing Blank Line separator, <400> field identifier  
L:62 M:283 W: Missing Blank Line separator, <220> field identifier  
L:63 M:283 W: Missing Blank Line separator, <400> field identifier  
L:70 M:283 W: Missing Blank Line separator, <220> field identifier  
L:71 M:283 W: Missing Blank Line separator, <400> field identifier  
L:108 M:283 W: Missing Blank Line separator, <220> field identifier  
L:109 M:283 W: Missing Blank Line separator, <400> field identifier  
L:121 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:8  
M:332 Repeated in SeqNo=8  
L:179 M:252 E: No. of Seq. differs, <211> LENGTH:Input:522 Found:512 SEQ:8  
L:185 M:283 W: Missing Blank Line separator, <220> field identifier  
L:186 M:283 W: Missing Blank Line separator, <400> field identifier  
L:224 M:283 W: Missing Blank Line separator, <220> field identifier  
L:225 M:283 W: Missing Blank Line separator, <400> field identifier  
L:238 M:332 E: (32) Invalid/Missing Amino Acid Numbering, SEQ ID:10  
M:332 Repeated in SeqNo=10  
L:265 M:283 W: Missing Blank Line separator, <220> field identifier  
L:266 M:283 W: Missing Blank Line separator, <400> field identifier  
L:273 M:283 W: Missing Blank Line separator, <220> field identifier  
L:274 M:283 W: Missing Blank Line separator, <400> field identifier  
L:281 M:283 W: Missing Blank Line separator, <220> field identifier  
L:282 M:283 W: Missing Blank Line separator, <400> field identifier  
L:289 M:283 W: Missing Blank Line separator, <220> field identifier  
L:290 M:283 W: Missing Blank Line separator, <400> field identifier  
L:298 M:283 W: Missing Blank Line separator, <220> field identifier  
L:299 M:283 W: Missing Blank Line separator, <400> field identifier  
L:300 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:27 SEQ:15  
L:309 M:283 W: Missing Blank Line separator, <220> field identifier  
L:310 M:283 W: Missing Blank Line separator, <400> field identifier  
L:317 M:283 W: Missing Blank Line separator, <220> field identifier  
L:318 M:283 W: Missing Blank Line separator, <400> field identifier  
L:319 M:254 E: No. of Bases conflict, LENGTH:Input:0 Counted:20 SEQ:17  
L:326 M:283 W: Missing Blank Line separator, <220> field identifier  
L:327 M:283 W: Missing Blank Line separator, <400> field identifier  
L:334 M:283 W: Missing Blank Line separator, <220> field identifier  
L:335 M:283 W: Missing Blank Line separator, <400> field identifier  
L:344 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5  
L:346 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:19

VERIFICATION SUMMARY

PATENT APPLICATION: US/10/026,106C

DATE: 10/08/2002

TIME: 13:59:25

Input Set : A:\EP.txt

Output Set: N:\CRF4\10082002\J026106C.raw

L:346 M:334 W: (2) Invalid Amino Acid in Coding Region, NUMBER OF INVALID KEYS:5